Search Notes

Application/Control No.	Applicant(s)/Patent under Reexamination
10/526,323	EBRIGHT, RICHARD H
Examiner	**Art Unit**
Julie Ha	1654

SEARCHED			
Class	Subclass	Date	Examiner
None			

INTERFERENCE SEARCHED			
Class	Subclass	Date	Examiner
None			

SEARCH NOTES (INCLUDING SEARCH STRATEGY)		
	DATE	EXMR
Updated EAST and PALM inventor search	10/10/2007	JH
Updated EAST: please see attached	10/10/2007	JH
Updated STN: please see attached	10/3/2007	JH

	Ref #	Hits	Search Text
1	S1	5	RNAP near5(secondary adj channel)
2	S2	20	((RNAP)near5(screen$ or identify$)).ab,clm.
3	S3	0	((RNAP)near5(screen$ or identify$)).ab,clm. same ((RNA) adj synthesis)
4	S4	0	((RNAP)near5(screen$ or identify$)).ab,clm. same ((RNA) adj synthes$)
5	S5	14	"6225076"
6	S6	15	((RNAP)near5(screen$ or identify$)).ab,clm. and (kinteic$ or bind$)
7	S7	11	((RNAP)near5(screen$ or identify$)).ab,clm. and (antibacterial$)
8	S8	1617	(microcin or (McbA protein) or (Mcc25 protein) or (MccJ25) or (MccB17) or (MccE492) or bacteriocin)
9	S9	3	S8 same RNAP near5 (secondary adj channel)
10	S10	3	S8 same (RNAP near5 (secondary adj channel))
11	S11	5	S8 and (RNAP near5 (secondary adj channel))
12	S12	0	S8 and (RNAP near5 (pore))
13	S13	1	(RNA polymerase) same (secondary channel)
14	S14	22	Ebright-richard-h.in.
15	S15	1	("20060160158").PN.

=> d l20 1-29 ibib, abs

L20 ANSWER 1 OF 29 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2000:375961 BIOSIS
DOCUMENT NUMBER: PREV200000375961
TITLE: O-glycosylation of nuclear proteins.
AUTHOR(S): Krzeslak, Anna [Reprint author]; Lipinska, Anna [Reprint author]
CORPORATE SOURCE: ul. S. Banacha 12/16, 90-237, Lodz, Poland
SOURCE: Postepy Biologii Komorki, (***2000***) Vol. 27, No. 3, pp. 441-460. print.
CODEN: PBKODV. ISSN: 0324-833X.
DOCUMENT TYPE: Article
LANGUAGE: Polish
ENTRY DATE: Entered STN: 6 Sep 2000
Last Updated on STN: 8 Jan 2002

AB Glycosylation, consisting in incorporation of single N-acetylglucosamine residues attached by O-linkage to serine or threonine residues, is a common modification of nuclear proteins. Numerous chromatin and nuclear ***pore*** complex proteins as well as ***RNA polymerase*** II and some transcription factors are glycosylated in this unusual way. O-glycosylation of nuclear proteins has been postulated to play a role in nucleus-cytoplasmic transport, transcriptional regulation and regulation of protein phosphorylation level. In this paper data concerning enzymes engaged in O-glycosylation and deglycosylation of proteins, attachment sites of N-acetylglucosamine residues and known nuclear glycoproteins have been described.

L20 ANSWER 2 OF 29 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2000:49957 BIOSIS
DOCUMENT NUMBER: PREV200000049957
TITLE: O-GlcNAc and the control of gene expression.
AUTHOR(S): Comer, Frank I.; Hart, Gerald W. [Reprint author]
CORPORATE SOURCE: Department of Biological Chemistry, Johns Hopkins University School of Medicine, 725 N. Wolfe St., Baltimore, MD, USA
SOURCE: Biochimica et Biophysica Acta, (***Dec. 6, 1999***) Vol. 1473, No. 1, pp. 161-171. print.
CODEN: BBACAQ. ISSN: 0006-3002.
DOCUMENT TYPE: Article
General Review; (Literature Review)
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Feb 2000
Last Updated on STN: 31 Dec 2001

AB Many eukaryotic proteins contain O-linked N-acetylglucosamine (O-GlcNAc) on their serine and threonine side chain hydroxyls. In contrast to classical cell surface glycosylation, O-GlcNAc occurs on resident nuclear and cytoplasmic proteins. O-GlcNAc exists as a single monosaccharide residue, showing no evidence of further elongation. Like phosphorylation, O-GlcNAc is highly dynamic, transiently modifying proteins. These post-translational modifications give rise to functionally distinct subsets of a given protein. Furthermore, all known O-GlcNAc proteins are also phosphoproteins that reversibly form multimeric complexes that are sensitive to the state of phosphorylation. This observation implies that O-GlcNAc may work in concert with phosphorylation to mediate regulated protein interactions. The proteins that bear the O-GlcNAc modification are very diverse, including ***RNA polymerase*** II and many of its transcription factors, numerous chromatin-associated proteins, nuclear ***pore*** proteins, proto-oncogenes, tumor suppressors and proteins involved in translation. Here, we discuss the functional implications of O-GlcNAc-modifications of proteins involved in various aspects of gene expression, beginning with proteins involved in transcription and ending with proteins involved in regulating protein

translation.

L20 ANSWER 3 OF 29 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 1995:135373 BIOSIS
DOCUMENT NUMBER: PREV199598149673
TITLE: The metabolism of small cellular RNA species during productive subgroup C adenovirus infection.
AUTHOR(S): Smiley, Jean K.; Young, Marjorie A.; Bansbach, Catherine C.; Flint, S. J. [Reprint author]
CORPORATE SOURCE: Dep. Mol. Biol., Princeton Univ., Princeton, NJ 08544-1014, USA
SOURCE: Virology, (*1995*) Vol. 206, No. 1, pp. 100-107.
CODEN: VIRLAX. ISSN: 0042-6822.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 29 Mar 1995
Last Updated on STN: 29 Mar 1995

AB During the late phase of subgroup C adenovirus infection, export of cellular mRNA from the nucleus to the cytoplasm is inhibited. In one approach to investigate the mechanism whereby viral late mRNAs are selected for export, we have examined the metabolism of small cellular RNA species transcribed by all three RNA polymerases during the late phase of Ad5 infection. No changes in the quantities of (3H)uridine-labeled 5S rRNA or tRNAs entering the cytoplasm were observed in infected cells. Adenovirus type 5 infection reduced the nuclear and cytoplasmic populations of the newly synthesized, snRNP-associated snRNAs U1, U2, U4, U5, and U6. Transcription of a representative snRNA, U1 RNA, was not inhibited, indicating that the post-transcriptional metabolism of snRNAs was perturbed during the late phase of infection. The increased cytoplasmic concentration of newly synthesized U1 RNA in Ad5- compared to mock-infected cells, and the greater reduction of the snRNP-associated compared to the total U1 RNA population, indicated that snRNP assembly in the cytoplasm was impaired. As adenovirus infection does not perturb export from the nucleus of small cellular mRNAs transcribed by ***RNA polymerases*** II and III, viral mRNA must be distinguished for selective export at a nuclear step upstream of translocation to the cytoplasm via nuclear ***pore*** complexes.

L20 ANSWER 4 OF 29 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 1994:500167 BIOSIS
DOCUMENT NUMBER: PREV199497513167
TITLE: An RNase-sensitive particle containing Drosophila melanogaster DNA topoisomerase II.
AUTHOR(S): Meller, Victoria H.; McConnell, Maeve; Fisher, Paul A. [Reprint author]
CORPORATE SOURCE: Dep. Pharmacol. Sci., University Med. Center, State University New York Stony Brook, NY 11794-8651, USA
SOURCE: Journal of Cell Biology, (*1994*) Vol. 126, No. 6, pp. 1331-1340.
CODEN: JCLBA3. ISSN: 0021-9525.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 28 Nov 1994
Last Updated on STN: 12 Jan 1995

AB Most DNA topoisomerase II (topo II) in cell-free extracts of 0-2-h old Drosophila embryos appears to be nonnuclear and remains in the supernatant after low-speed centrifugation (10,000 g). Virtually all of this apparently soluble topo II is particulate with a sedimentation coefficient of 67 S. Similar topo II-containing particles were detected in Drosophila K-c tissue culture cells, 16-19-h old embryos and extracts of progesterone-matured oocytes from Xenopus. Drosophila topo II-containing particles were insensitive to EDTA, Triton X-100 and DNase 1, but could be disrupted by incubation with 0.3 M NaCl or RNase A. After either disruptive treatment, topo II sedimented at 9 S. topo II-containing

particles were also sensitive to micrococcal nuclease. Results of chemical crosslinking corroborated those obtained by centrifugation. Immunoblot analyses demonstrated that topo II-containing particles lacked significant amounts of lamin, nuclear ***pore*** complex protein gp210, proliferating cell nuclear antigen, ***RNA polymerase*** II subunits, histones, coilin, and nucleolin. Northern blot analyses demonstrated that topo II-containing particles lacked U RNA. Thus, current data support the notion that nonnuclear Drosophila topo II-containing particles are composed largely of topo II and an unknown RNA molecule(s).

L20 ANSWER 5 OF 29 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 1994:400541 BIOSIS
DOCUMENT NUMBER: PREV199497413541
TITLE: Yeast Srp1p has homology to armadillo/plakoglobin/beta-catenin and participates in apparently multiple nuclear functions including the maintenance of the nucleolar structure.
AUTHOR(S): Yano, Ryoji [Reprint author]; Oakes, Melanie L.; Tabb, Michelle M.; Nomura, Masayasu
CORPORATE SOURCE: Lab. Neural Networks, Frontier Res. Program, Inst. Physical Chemical Res., Wako, Saitama 351-01, Japan
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (***1994***) Vol. 91, No. 15, pp. 6880-6884.
CODEN: PNASA6. ISSN: 0027-8424.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 23 Sep 1994
Last Updated on STN: 23 Sep 1994

AB SRP1, a suppressor of certain temperature-sensitive mutations in ***RNA polymerase*** I in Saccharomyces cerevisiae, encodes a protein that is associated with nuclear ***pores***. By using a system of conditional SRP1 expression and by isolating temperature-sensitive srp1 mutants, we have demonstrated that Srp1p is essential for maintenance of the crescent-shaped nucleolar structure, RNA transcription, and the proper functions of microtubules as inferred from analysis of nuclear division/segregation and immunofluorescence microscopy of microtubules. Different mutant alleles showed significantly different phenotypes in relation to these apparently multiple functional roles of the protein. We have also found that eight imperfect 42-amino-acid tandem repeats present in Srp1p are similar to the 42-amino-acid repeats in armadillo/plakoglobin/beta-catenin proteins present in adhesive junction complexes of higher eucaryotes. We discuss this similarity in connection with the observed pleiotropic effects of srp1 mutations.

L20 ANSWER 6 OF 29 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 1992:274541 BIOSIS
DOCUMENT NUMBER: PREV199242133491; BR42:133491
TITLE: GLYCOSYLATION OF NUCLEAR PROTEINS A DYNAMIC AND POSSIBLY REGULATORY MODIFICATION.
AUTHOR(S): HART G W [Reprint author]; HALTIWANGER R S; BLOMBERG M A; KELLY W G; ROQUEMORE E; DONG L-Y D
CORPORATE SOURCE: DEP BIOL CHEM, JOHNS HOPKINS UNIV SCH MED, 725 N WOLFE ST, BALTIMORE, MD 21205, USA
SOURCE: Abstracts of Papers American Chemical Society, (***1992***) Vol. 203, No. 1-3, pp. CARB4.
Meeting Info.: 203RD ACS (AMERICAN CHEMICAL SOCIETY) NATIONAL MEETING, SAN FRANCISCO, CALIFORNIA, USA, APRIL 5-10, 1992. ABSTR PAP AM CHEM SOC.
CODEN: ACSRAL. ISSN: 0065-7727.
DOCUMENT TYPE: Conference; (Meeting)
FILE SEGMENT: BR
LANGUAGE: ENGLISH

ENTRY DATE: Entered STN: 31 May 1992
Last Updated on STN: 31 May 1992

L20 ANSWER 7 OF 29 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 1991:249147 BIOSIS
DOCUMENT NUMBER: PREV199191129702; BA91:129702
TITLE: STRUCTURE OF THE MOUSE PORE-FORMING PROTEIN PERFORIN GENE ANALYSIS OF TRANSCRIPTION INITIATION SITE 5' FLANKING SEQUENCE AND ALTERNATIVE SPLICING OF 5' UNTRANSLATED REGIONS.
AUTHOR(S): YOUN B-S [Reprint author]; LIU C-C; KIM K-K; YOUNG J D-E; KWON M H; KWON B S
CORPORATE SOURCE: DEP MICROBIOL IMMUNOL, WALTHER ONCOL CENT, INDIANA UNIV SCH MED, 635 BARNHILL DR, INDIANAPOLIS, INDIANA 46202, USA
SOURCE: Journal of Experimental Medicine, (*1991*) Vol. 173, No. 4, pp. 813-822.
CODEN: JEMEAV. ISSN: 0022-1007.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH
OTHER SOURCE: GENBANK-X56613
ENTRY DATE: Entered STN: 25 May 1991
Last Updated on STN: 25 May 1991

AB We studied the 5' untranslated regions (UTRs) of the mouse lymphocyte ***pore***-forming protein (PFP, perforin, and cytalysin). 5' UTRs were determined by primers extension analysis, sequencing PFP cDNA clone PFP-7, ribonuclease protection assays, and amplification of poly(A)+ ***RNA*** of cytolytic T lymphocyte using ***polymerase*** chain reaction (PCR). Two alternatively spliced 5' UTRs, designated type I and type II, of 222 and 115 bp, respectively, were found associated with PFP. Type II is identical to type I, except for being 107 bp shorter in the second exon. This deletion was generated by the use of alternative acceptor splice sites. The mouse PFP gene (Pfp) encodes three exons, is separated by two small introns, and spans a chromosomal region of .apprx. 7 kb. The first exon contains 79 bp of 5' UTR, the second exon contains 143 or 36 bp of 5' UTR (type I or type II UTR, respectively) plus the NH2-terminal region of the mouse PFP, and the third exon contains the rest of the COOH-terminal mouse PFP. The organization of the mouse Pfp is highly homologous to that of the human Pfp. In contrast to the human sequence, the more immediate 5' flanking sequence of mouse Pfp contains two tandem "TATA" box-related elements and a GC box, but lacks a typical CAAT box-related sequence. Several other enhancer elements were found further upstream, including cAMP-, phorbol ester-, interferon-γ-, and UV-responsive elements, and PU box-like and NFkB binding site-like elements. In addition, we found a nuclear inhibitory-protein-like element, a transcriptional silencer, and a pair of purine-rich sequence motifs that were found in other T cell-specific genes, and three repeats of GGCCTG that may be a variation of a highly repetitious GCCCTG consensus sequence found in human Pfp.

L20 ANSWER 8 OF 29 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
ACCESSION NUMBER: 2000224156 EMBASE
TITLE: Engines of gene expression.
AUTHOR: Geiduschek E.P.; Bartlett M.S.
CORPORATE SOURCE: E.P. Geiduschek, Department of Biology, University of California, 9500 Gilman Drive, San Diego, CA 92093-0634, United States. epg@biomail.ucsd.edu
SOURCE: Nature Structural Biology, (Jun 2000) Vol. 7, No. 6, pp. 437-439.
Refs: 20
ISSN: 1072-8368 CODEN: NSBIEW
COUNTRY: United States
DOCUMENT TYPE: Journal; (Short Survey)

FILE SEGMENT: 004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 13 Jul 2000
Last Updated on STN: 13 Jul 2000

AB A backbone model of ten subunits of yeast RNA polymerase II has been derived from the ongoing analysis of its crystal structure. Notable features include 'jaws' for holding DNA, a putatively RNA-regulated 'sliding clamp', two '***pores***' located in the vicinity of the catalytic center, and a high degree of similarity with the structure of a bacterial ***RNA polymerase***.

L20 ANSWER 9 OF 29 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
ACCESSION NUMBER: 1999411322 EMBASE
TITLE: O-GlcNAc and the control of gene expression.
AUTHOR: Comer F.I.; Hart G.W.
CORPORATE SOURCE: G.W. Hart, Department of Biological Chemistry, Johns Hopkins Univ. Sch. of Medicine, 725 N. Wolfe St., Baltimore, MD 21205, United States. gwhart@bs.jhmi.edu
SOURCE: Biochimica et Biophysica Acta - General Subjects, (17 Dec 1999) Vol. 1473, No. 1, pp. 161-171.
Refs: 56
ISSN: 0304-4165 CODEN: BBGSB3
PUBLISHER IDENT.: S 0304-4165(99)00176-2
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; General Review; (Review)
FILE SEGMENT: 029 Clinical and Experimental Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 16 Dec 1999
Last Updated on STN: 16 Dec 1999

AB Many eukaryotic proteins contain O-linked N-acetylglucosamine (O-GlcNAc) on their serine and threonine side chain hydroxyls. In contrast to classical cell surface glycosylation, O-GlcNAc occurs on resident nuclear and cytoplasmic proteins. O-GlcNAc exists as a single monosaccharide residue, showing no evidence of further elongation. Like phosphorylation, O-GlcNAc is highly dynamic, transiently modifying proteins. These post-translational modifications give rise to functionally distinct subsets of a given protein. Furthermore, all known O-GlcNAc proteins are also phosphoproteins that reversibly form multimeric complexes that are sensitive to the state of phosphorylation. This observation implies that O-GlcNAc may work in concert with phosphorylation to mediate regulated protein interactions. The proteins that bear the O-GlcNAc modification are very diverse, including ***RNA polymerase*** II and many of its transcription factors, numerous chromatin- associated proteins, nuclear ***pore*** proteins, proto-oncogenes, tumor suppressors and proteins involved in translation. Here, we discuss the functional implications of O-GlcNAc-modifications of proteins involved in various aspects of gene expression, beginning with proteins involved in transcription and ending with proteins involved in regulating protein translation.

L20 ANSWER 10 OF 29 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
ACCESSION NUMBER: 1997195532 EMBASE
TITLE: Dynamic O-linked glycosylation of nuclear and cytoskeletal proteins.
AUTHOR: Hart G.W.
CORPORATE SOURCE: G.W. Hart, Dept. of Biochem./Molec. Genetics, University of Alabama, Schools of Medicine and Dentistry, Birmingham, AL 35294-0005, United States. gwhart@bmg.bhs.uab.edu
SOURCE: Annual Review of Biochemistry, (1997) Vol. 66, pp. 315-335.

Refs: 190
ISSN: 0066-4154 CODEN: ARBOAW
COUNTRY: United States
DOCUMENT TYPE: Journal; General Review; (Review)
FILE SEGMENT: 026 Immunology, Serology and Transplantation
029 Clinical and Experimental Biochemistry
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 7 Aug 1997
Last Updated on STN: 7 Aug 1997

AB Modification of Ser and Thr residues by attachment of O-linked N-acetylglucosamine [Ser(Thr)-O-GlcNAcylation] to eukaryotic nuclear and cytosolic proteins is as dynamic and possibly as abundant as Ser(Thr) phosphorylation. Known O-GlcNAcylated proteins include cytoskeletal proteins and their regulatory proteins; viral proteins; nuclear-***pore***, heat-shock, tumor-suppressor, and nuclear-oncogene proteins; ***RNA polymerase*** II catalytic subunit; and a multitude of transcription factors. Although functionally diverse, all of these proteins are also phosphoproteins. Most O-GlcNAcylated proteins form highly regulated multimeric associations that are dependent upon their posttranslational modifications. Evidence is mounting that O-GlcNAcylation is an important regulatory modification that may have a reciprocal relationship with O-phosphorylation and may modulate many biological processes in eukaryotes.

L20 ANSWER 11 OF 29 EMBASE
ACCESSION NUMBER: 1995043467 EMBASE
TITLE: The metabolism of small cellular RNA species during productive subgroup C adenovirus infection.
AUTHOR: Smiley J.K.; Young M.A.; Bansbach C.C.; Flint S.J.
CORPORATE SOURCE: C.C. Bansbach, Department of Molecular Biology, Princeton University, Princeton, NJ 08544-1014, United States
SOURCE: Virology, (1995) Vol. 206, No. 1, pp. 100-107.
ISSN: 0042-6822 CODEN: VIRLAX
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 8 Mar 1995
Last Updated on STN: 8 Mar 1995

AB During the late phase of subgroup C adenovirus infection, export of cellular mRNA from the nucleus to the cytoplasm is inhibited. In one approach to investigate the mechanism whereby viral late mRNAs are selected for export, we have examined the metabolism of small cellular RNA species transcribed by all three RNA polymerases during the late phase of Ad5 infection. No changes in the quantities of [(3)H]uridine-labeled 5S rRNA or tRNAs entering the cytoplasm were observed in infected cells. Adenovirus type 5 infection reduced the nuclear and cytoplasmic populations of the newly synthesized, snRNP-associated snRNAs U1, U2, U4, U5, and U6. Transcription of a representative snRNA, U1 RNA, was not inhibited, indicating that the post-transcriptional metabolism of snRNAs was perturbed during the late phase of infection. The increased cytoplasmic concentration of newly synthesized U1 RNA in Ad5-compared to mock-infected cells, and the greater reduction of the snRNP-associated compared to the total U1 RNA population, indicated that snRNP assembly in the cytoplasm was impaired. As adenovirus infection does not perturb export from the nucleus of small cellular mRNAs transcribed by ***RNA polymerases*** II and III, viral mRNA must be distinguished for selective export at a nuclear step upstream of translocation to the

cytoplasm via nuclear ***pore*** complexes.

L20 ANSWER 12 OF 29 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN

ACCESSION NUMBER: 1994289142 EMBASE
TITLE: An RNase-sensitive particle containing Drosophila melanogaster DNA topoisomerase II.
AUTHOR: Meller V.H.; McConnell M.; Fisher P.A.
CORPORATE SOURCE: Dr. P.A. Fisher, Pharmacological Sciences Department, University Medical Center, State University of New York, Stony Brook, NY 11794-8651, United States
SOURCE: Journal of Cell Biology, (Sep 1994) Vol. 126, No. 6, pp. 1331-1340.
Refs: 59
ISSN: 0021-9525 CODEN: JCLBA3
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 029 Clinical and Experimental Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 13 Oct 1994
Last Updated on STN: 13 Oct 1994

AB Most DNA topoisomerase II (topo II) in cell-free extracts of 0-2 h old Drosophila embryos appears to be nonnuclear and remains in the supernatant after low-speed centrifugation (10,000 g). Virtually all of this apparently soluble topo II is particulate with a sedimentation coefficient of 67 S. Similar topo II-containing particles were detected in Drosophila K(c) tissue culture cells, 16-19-h old embryos and extracts of progesterone-matured oocytes from Xenopus. Drosophila topo II-containing particles were insensitive to EDTA, Triton X-100 and DNase I, but could be disrupted by incubation with 0.3 M NaCl or RNase A. After either disruptive treatment, topo II sedimented at 9 S. topo II-containing particles were also sensitive to micrococcal nuclease. Results of chemical cross-linking corroborated those obtained by centrifugation. Immunoblot analyses demonstrated that topo II- containing particles lacked significant amounts of lamin, nuclear ***pore*** complex protein gp210, proliferating cell nuclear antigen, ***RNA polymerase*** II subunits, histones, coilin, and nucleolin. Northern blot analyses demonstrated that topo II-containing particles lacked U RNA. Thus, current data support the notion that nonnuclear Drosophila topo II-containing particles are composed largely of topo II and an unknown RNA molecule(s).

L20 ANSWER 13 OF 29 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN

ACCESSION NUMBER: 1994233429 EMBASE
TITLE: Yeast Srp1p has homology to armadillo/plakoglobin/β-catenin and participates in apparently multiple nuclear functions including the maintenance of the nucleolar structure.
AUTHOR: Yano R.; Oakes M.L.; Tabb M.M.; Nomura M.
CORPORATE SOURCE: R. Yano, Frontier Research Program, Laboratory for Neural Networks, Physical/Chemical Research Institute, Wako, Saitama 351-01, Japan
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (19 Jul 1994) Vol. 91, No. 15, pp. 6880-6884.
Refs: 22
ISSN: 0027-8424 CODEN: PNASA6
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical and Experimental Biochemistry
LANGUAGE: English

SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 17 Aug 1994
Last Updated on STN: 17 Aug 1994

AB SRP1, a suppressor of certain temperature-sensitive mutations in ***RNA polymerase*** I in Saccharomyces cerevisiae, encodes a protein that is associated with nuclear ***pores***. By using a system of conditional SRP1 expression and by isolating temperature-sensitive srp1 mutants, we have demonstrated that Srp1p is essential for maintenance of the crescent-shaped nucleolar structure, RNA transcription, and the proper functions of microtubules as inferred from analysis of nuclear division/segregation and immunofluorescence microscopy of microtubules. Different mutant alleles showed significantly different phenotypes in relation to these apparently multiple functional roles of the protein. We have also found that eight imperfect 42-amino-acid tandem repeats present in Srp1p are similar to the 42-amino-acid repeats in armadillo/plakoglobin/β-catenin proteins present in adhesive junction complexes of higher eukaryotes. We discuss this similarity in connection with the observed pleiotropic effects of srp1 mutations.

L20 ANSWER 14 OF 29 EMBASE
ACCESSION NUMBER: 1991149489 EMBASE
TITLE: Structure of the mouse pore-forming protein (perforin) gene: Analysis of transcription initiation site, 5' flanking sequence, and alternative splicing of 5' untranslated regions.
AUTHOR: Youn B.-S.; Liu C.-C.; Kim K.-K.; Young J.D.-E.; Kwon M.H.; Kwon B.S.
CORPORATE SOURCE: B.S. Kwon, Microbiology/Immunology Dept., Walther Oncology Center, Indiana Univ. Sch. of Medicine, 635 Barnhill Drive, Indianapolis, IN 46202, United States
SOURCE: Journal of Experimental Medicine, (1991) Vol. 173, No. 4, pp. 813-822.
ISSN: 0022-1007 CODEN: JEMEAV
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 16 Dec 1991
Last Updated on STN: 16 Dec 1991

AB We studied the 5' untranslated regions (UTRs) of the mouse lymphocyte ***pore***-forming protein (PFP, perforin, and cytolysin). 5' UTRs were determined by primer extension analysis, sequencing PFP cDNA clone PFP-7, ribonuclease protection assays, and amplification of poly(A)(+) ***RNA*** of cytolytic T lymphocyte using ***polymerase*** chain reaction (PCR). Two alternatively spliced 5' UTRs, designated type I and type II, of 222 and 115 bp, respectively, were found associated with PFP. Type II is identical to type I, except for being 107 bp shorter in the second exon. This deletion was generated by the use of alternative acceptor splice sites. The mouse PFP gene (Pfp) encodes three exons, is separated by two small introns, and spans a chromosomal region of 7 kb. The first exon contains 79 bp of 5' UTR, the second exon contains 143 or 36 bp of 5' UTR (type I or type II UTR, respectively) plus the NH(2)-terminal region of the mouse PFP, and the third exon contains the rest of the COOH-terminal mouse PFP. The organization of the mouse Pfp is similar to that of the human gene. Moreover, the 5' flanking sequence of the mouse Pfp is highly homologous to that of the human Pfp. In contrast to the human sequence, the more immediate 5' flanking sequence of mouse Pfp contains two tandem 'TATA' box-related elements and a GC box, but lacks a typical CAAT box-related sequence. Several other enhancer elements were found further upstream, including cAMP-, phorbol ester-, interferon-γ-, and UV-responsive elements, and PU box-like and NFkB binding site-like elements. In addition, we found a nuclear inhibitory